

SEQUENCE LISTING

<110> COLE, Stewart
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<120> DELETED SEQUENCE IN M. TUBERCULOSIS, METHOD FOR
DETECTING MYCOBACTERIA USING THESE SEQUENCES AND
VACCINES

<130> 346 379- US

<150> PCT/IB 03/00 986

<151> 2003-02-25

<150> EP 02/290 458

<151> 2002-02-25

<160> 22

<170> PatentIn Ver. 2.1

<210> 1

<211> 3953

<212> DNA

<213> Mycobacterium tuberculosis strain 74 ("ancestral" strain)

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Pro	Asp	Phe	Gln	Arg	Gly	Leu	Lys	Leu	Phe	Leu	Ser	Ala	Asp	Gly	Lys	
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Ala	His	Thr	Pro	Pro	Pro	Ala	Gly	Val	Lys	Ala	Tyr	Val	Thr	Gly	Ala	165	170	175	
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Lys	Val	Thr	Gly	Ile	Thr	Leu	Val	Val	Ile	Ala	Val	Met	Leu	Leu	Phe	195	200	205	
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<213> Mycobacterium tuberculosis strain 74 ("ancestral" strain)

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Asp Ala Thr Pro Arg Gln Val Leu Asp Thr Thr Leu Pro Trp Ser Tyr
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Arg Leu Ser Leu Pro Ile Leu Leu Phe Trp Val Gly Val Ala Ala Ile	
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acc aat gcc gcc gtg ccg caa ttg gag gtg gtc ggg gag gcg cat aac	144
Thr Asn Ala Ala Val Pro Gln Leu Glu Val Val Gly Glu Ala His Asn	
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gtc gca cag agc tcc ccg gat gac ccg tcg ctg cag gcg atg aaa cgc	192
Val Ala Gln Ser Ser Pro Asp Asp Pro Ser Leu Gln Ala Met Lys Arg	
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atc ggc aag gtg ttc cac gag ttc gat tcc gac agt gcg gcc atg atc	240
Ile Gly Lys Val Phe His Glu Phe Asp Ser Asp Ser Ala Ala Met Ile	
65 70 75 80	
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Val Leu Glu Gly Asp Lys Pro Leu Gly Asn Asp Ala His Arg Phe Tyr	
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Asp Thr Leu Leu Arg Asn Leu Ser Asn Asp Thr Lys His Val Glu His	
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gtt cag gac ttc tgg ggc gat ccg ctg acc gcg gcc ggc tcg caa agc	384
Val Gln Asp Phe Trp Gly Asp Pro Leu Thr Ala Ala Gly Ser Gln Ser	
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acc gac ggc aaa gcc gcc tac gtt cag gtc tat ctc gcc ggc aac caa	432
Thr Asp Gly Lys Ala Ala Tyr Val Gln Val Tyr Leu Ala Gly Asn Gln	
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Gly Glu Ala Leu Ser Ile Glu Ser Val Asp Ala Val Arg Asp Ile Val	
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Ala His Thr Pro Pro Ala Gly Val Lys Ala Tyr Val Thr Gly Ala	
165 170 175	
gcc ccg ctc atg gcc gat cag ttt cag gtg ggc agc aaa gga acc gcg	576
Ala Pro Leu Met Ala Asp Gln Phe Gln Val Gly Ser Lys Gly Thr Ala	
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aaa gtt acc ggg ata act ctg gtt gtg atc gcg gtg atg ttg ctc ttc	624
Lys Val Thr Gly Ile Thr Leu Val Val Ile Ala Val Met Leu Leu Phe	
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gta tac cgt tcc gtc gtc acc atg gtc ctg gtg ctt atc acg gtt ctt	672
Val Tyr Arg Ser Val Val Thr Met Val Leu Val Leu Ile Thr Val Leu	
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gta atc gcg gcg ggc aca gac tac gcg att ttt gtc ctc ggc cgc tat	816
Val Ile Ala Ala Gly Thr Asp Tyr Ala Ile Phe Val Leu Gly Arg Tyr	
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His Glu Ala Arg Tyr Ala Ala Gln Asp Arg Glu Thr Ala Phe Tyr Thr	
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Met Tyr Arg Gly Thr Ala His Val Val Leu Gly Ser Gly Leu Thr Val	
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Ala Gly Ala Val Tyr Cys Leu Ser Phe Thr Arg Leu Pro Tyr Phe Gln	
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agc ctg ggt att ccc gcc tcg ata ggg gtg atg att gcg ttg gca gcc	1008
Ser Leu Gly Ile Pro Ala Ser Ile Gly Val Met Ile Ala Leu Ala Ala	
325 330 335	
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Cys Phe Glu Pro Lys Arg Arg Met Arg Thr Arg Gly Trp Arg Arg Ile	
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Gly Thr Ala Ile Val Arg Trp Pro Gly Pro Ile Leu Ala Val Ala Cys	
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Ala Ile Ala Val Val Gly Leu Leu Ala Leu Pro Gly Tyr Lys Thr Ser	
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Tyr Asp Ala Arg Tyr Tyr Met Pro Ala Thr Ala Pro Ala Asn Ile Gly	
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Tyr Met Ala Ala Glu Arg His Phe Pro Gln Ala Arg Leu Asn Pro Glu	
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Leu Leu Met Ile Glu Thr Asp His Asp Met Arg Asn Pro Ala Asp Met	
435 440 445	
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Leu Ile Leu Asp Arg Ile Ala Lys Ala Val Phe His Leu Pro Gly Ile	
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Gly Leu Val Gln Ala Met Thr Arg Pro Leu Gly Thr Pro Ile Asp His	
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Glu Glu Leu Gly Lys Thr Ile Glu Ile Leu Gln Arg Gln Tyr Ala Leu	
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Gln Gln Glu Leu Ala Ala Thr His Glu Gln Ala Glu Ser Phe His	
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Cys Tyr Asp Ile Pro Ser Cys Trp Ala Leu Arg Ser Val Phe Asp Thr	
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Thr Leu Asp Lys Leu Ala Ala Ile Gln Pro Gln Leu Val Ala Leu Leu	
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Pro Asp Glu Ile Ala Ser Gln Gln Ile Asn Arg Glu Leu Ala Leu Ala	
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aac tac gcc acc atg tcc ggg atc tat gcc cag acg gcg gcc ttg atc	1968
Asn Tyr Ala Thr Met Ser Gly Ile Tyr Ala Gln Thr Ala Ala Leu Ile	
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gaa aac gct gcc gcc atg gga caa gcc ttt gac gcc gcc aag aac gac	2016
Glu Asn Ala Ala Ala Met Gly Gln Ala Phe Asp Ala Ala Lys Asn Asp	
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gac tcc ttc tat ctg ccg ccg gag gct ttt gac aac cca gat ttc cag	2064
Asp Ser Phe Tyr Leu Pro Pro Glu Ala Phe Asp Asn Pro Asp Phe Gln	
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gcg	ctg	agc	ttg	att	ttg	ctc	atc	atg	atg	atc	att	acc	cga	agc	ctg	2352	
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Leu	Tyr	Trp	Ile	Val	Leu	Ala	Leu	Ala	Val	Ile	Leu	Leu	Leu	Ala	Val		
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Gly	Val	Val	Thr	Ala	Ala	Gly	Leu	Val	Phe	Ala	Ala	Thr	Met	Ser	Ser		
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ttc	gtg	ttc	agt	gat	ttg	cgg	gtc	ctc	ggt	cag	atc	ggg	acc	acc	att	2688	
Phe	Val	Phe	Ser	Asp	Leu	Arg	Val	Leu	Gly	Gln	Ile	Gly	Thr	Thr	Ile		
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ggt	ctt	ggg	ctg	ctg	ttc	gac	acg	ctg	gtg	gtg	cgc	gcg	ttc	atg	acc	2736	
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Val	Arg	Pro	Arg	Pro	Ala	Ser	Arg	Met	Leu	Arg	Pro	Tyr	Gly	Pro	Arg		
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ccc	gtg	gtt	cgt	gaa	ttg	ctg	ctg	cgc	gag	ggc	aac	gat	gac	ccg	aga	2880	
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 Val Ala Gln Ser Ser Pro Asp Asp Pro Ser Leu Gln Ala Met Lys Arg
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 Ile Gly Lys Val Phe His Glu Phe Asp Ser Asp Ser Ala Ala Met Ile
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 Val Leu Glu Gly Asp Lys Pro Leu Gly Asn Asp Ala His Arg Phe Tyr
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 Thr Asp Gly Lys Ala Ala Tyr Val Gln Val Tyr Leu Ala Gly Asn Gln
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 Gly Glu Ala Leu Ser Ile Glu Ser Val Asp Ala Val Arg Asp Ile Val
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 Ala His Thr Pro Pro Pro Ala Gly Val Lys Ala Tyr Val Thr Gly Ala
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 Ala Pro Leu Met Ala Asp Gln Phe Gln Val Gly Ser Lys Gly Thr Ala
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 Lys Val Thr Gly Ile Thr Leu Val Val Ile Ala Val Met Leu Leu Phe
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 Val Tyr Arg Ser Val Val Thr Met Val Leu Val Leu Ile Thr Val Leu
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 Ile Glu Leu Ala Ala Ala Arg Gly Ile Val Ala Phe Leu Gly Asn Ala
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 Gly Val Ile Gly Leu Ser Thr Tyr Ser Thr Asn Leu Leu Thr Leu Leu
 245 250 255

Val Ile Ala Ala Gly Thr Asp Tyr Ala Ile Phe Val Leu Gly Arg Tyr
 260 265 270
 His Glu Ala Arg Tyr Ala Ala Gln Asp Arg Glu Thr Ala Phe Tyr Thr
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 Met Tyr Arg Gly Thr Ala His Val Val Leu Gly Ser Gly Leu Thr Val
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 Ala Gly Ala Val Tyr Cys Leu Ser Phe Thr Arg Leu Pro Tyr Phe Gln
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 Cys Phe Glu Pro Lys Arg Arg Met Arg Thr Arg Gly Trp Arg Arg Ile
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 Ser Ser Ile Pro Phe Gln Ile Ser Met Gln Ser Val Gly Gln Ile Gln
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Phe	Val	Phe	Ser	Asp	Leu	Arg	Val	Leu	Gly	Gln	Ile	Gly	Thr	Thr	Ile
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Val Arg Pro Arg Pro Ala Ser Arg Met Leu Arg Pro Tyr Gly Pro Arg		
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Met Ser Asn His His Arg Pro Arg Pro Trp Leu Pro His Thr Ile Arg	
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cgg ctt tcg ttg ccg atc ttg ctg ttt tgg gtg ggt gtg gcc gcc ata	96
Arg Leu Ser Leu Pro Ile Leu Leu Phe Trp Val Gly Val Ala Ala Ile	
20 25 30	
acc aat gcc gcc gtg ccg caa ttg gag gtg gtc ggg gag gcg cat aac	144
Thr Asn Ala Ala Val Pro Gln Leu Glu Val Val Gly Glu Ala His Asn	
35 40 45	
gtc gca cag agc tcc ccg gat gac ccg tcg ctg cag gcg atg aaa cgc	192
Val Ala Gln Ser Ser Pro Asp Asp Pro Ser Leu Gln Ala Met Lys Arg	
50 55 60	
atc ggc aag gtg ttc cac gag ttc gat tcc gac agt gcg gcc atg atc	240
Ile Gly Lys Val Phe His Glu Phe Asp Ser Asp Ser Ala Ala Met Ile	
65 70 75 80	
gtc ttg gaa ggc gat aag ccg ctc ggc aac gac gcc cac cgg ttc tac	288
Val Leu Glu Gly Asp Lys Pro Leu Gly Asn Asp Ala His Arg Phe Tyr	
85 90 95	
gac acc ctg ctc cgc aac ctt tca aac gac acc aaa cac gtc gag cac	336
Asp Thr Leu Leu Arg Asn Leu Ser Asn Asp Thr Lys His Val Glu His	
100 105 110	
gtt cag gac ttc tgg ggc gat ccg ctg acc gcg gcc ggc tcg caa agc	384
Val Gln Asp Phe Trp Gly Asp Pro Leu Thr Ala Ala Gly Ser Gln Ser	
115 120 125	

acc gac ggc aaa gcc gcc tac gtt cag gtc tat ctc gcc ggc aac caa	432
Thr Asp Gly Lys Ala Ala Tyr Val Gln Val Tyr Leu Ala Gly Asn Gln	
130 135 140	
ggc gag gcg ttg tca atc gag tcc gtc gac gcg gtg cgc gac atc gtc	480
Gly Glu Ala Leu Ser Ile Glu Ser Val Asp Ala Val Arg Asp Ile Val	
145 150 155 160	
gcc cat acg cca cca ccg gcc ggg gtc aag gcc tac gtc acc ggc gcg	528
Ala His Thr Pro Pro Pro Ala Gly Val Lys Ala Tyr Val Thr Gly Ala	
165 170 175	
gcc ccg ctc atg gcc gat cag ttt cag gtg ggc agc aaa gga acc gcg	576
Ala Pro Leu Met Ala Asp Gln Phe Gln Val Gly Ser Lys Gly Thr Ala	
180 185 190	
aaa gtt acc ggg ata act ctg gtt gtg atc gcg gtg atg ttg ctc ttc	624
Lys Val Thr Gly Ile Thr Leu Val Val Ile Ala Val Met Leu Leu Phe	
195 200 205	
gta tac cgt tcc gtc gtc acc atg gtc ctg gtg ctt atc acg gtt ctt	672
Val Tyr Arg Ser Val Val Thr Met Val Leu Val Leu Ile Thr Val Leu	
210 215 220	
att gag ttg gcc gcg gcc cgc ggg atc gtc gct ttt ctc gga aac gcc	720
Ile Glu Leu Ala Ala Ala Arg Gly Ile Val Ala Phe Leu Gly Asn Ala	
225 230 235 240	
ggg gta atc ggg ctg tcg aca tac tcg acg aat ctg ctc aca cta ttg	768
Gly Val Ile Gly Leu Ser Thr Tyr Ser Thr Asn Leu Leu Thr Leu Leu	
245 250 255	
gta atc gcg gcg ggc aca gac tac gcg att ttt gtc ctc ggc cgc tat	816
Val Ile Ala Ala Gly Thr Asp Tyr Ala Ile Phe Val Leu Gly Arg Tyr	
260 265 270	
cac gag gcg cgc tac gcc gca cag gat cgg gaa acg gcc ttc tac acg	864
His Glu Ala Arg Tyr Ala Ala Gln Asp Arg Glu Thr Ala Phe Tyr Thr	
275 280 285	
atg tat cgc ggg acc gcc cac gtc gtc ttg ggc tcg ggt ctg acc gtt	912
Met Tyr Arg Gly Thr Ala His Val Val Leu Gly Ser Gly Leu Thr Val	
290 295 300	
gcc ggc gcg gtg tat tgc ctg agc ttt acc cgg cta ccc tat ttt caa	960
Ala Gly Ala Val Tyr Cys Leu Ser Phe Thr Arg Leu Pro Tyr Phe Gln	
305 310 315 320	
agc ctg ggt att ccc gcc tcg ata ggg gtg atg att gcg ttg gca gcc	1008
Ser Leu Gly Ile Pro Ala Ser Ile Gly Val Met Ile Ala Leu Ala Ala	
325 330 335	
gcg ctc agc ctg gcc cca tcc gtg ctc atc ttg ggc agt cgt ttc ggt	1056
Ala Leu Ser Leu Ala Pro Ser Val Leu Ile Leu Gly Ser Arg Phe Gly	
340 345 350	
tgt ttc gaa ccc aag cgc agg atg agg acc agg gga tgg cgg cgc atc	1104
Cys Phe Glu Pro Lys Arg Arg Met Arg Thr Arg Gly Trp Arg Arg Ile	
355 360 365	
ggc acg gcc atc gtg cgt tgg ccg gga ccc atc ctg gca gtg gcg tgc	1152

Gly	Thr	Ala	Ile	Val	Arg	Trp	Pro	Gly	Pro	Ile	Leu	Ala	Val	Ala	Cys.		
370						375					380						
gca	att	gcg	gtg	gtg	ggt	ctg	ctc	gcg	ctg	ccg	gga	tac	aaa	acg	agc	1200	
Ala	Ile	Ala	Val	Val	Gly	Leu	Leu	Ala	Leu	Pro	Gly	Tyr	Lys	Thr	Ser		
385					390					395					400		
tac	gac	gct	cg	tat	tac	atg	ccc	gcc	acc	gcc	ccg	gcc	aat	att	ggc	1248	
Tyr	Asp	Ala	Arg	Tyr	Tyr	Met	Pro	Ala	Thr	Ala	Pro	Ala	Asn	Ile	Gly		
				405					410					415			
tac	atg	gcc	gcg	gag	cga	cat	ttt	ccc	caa	gcg	cg	ctg	aat	ccc	gaa	1296	
Tyr	Met	Ala	Ala	Glu	Arg	His	Phe	Pro	Gln	Ala	Arg	Leu	Asn	Pro	Glu		
				420				425						430			
cta	ctg	atg	atc	gag	acg	gat	cac	gat	atg	cg	aat	ccg	gcc	gac	atg	1344	
Leu	Leu	Met	Ile	Glu	Thr	Asp	His	Asp	Met	Arg	Asn	Pro	Ala	Asp	Met		
				435			440					445					
ctc	atc	ttg	gat	agg	atc	gcc	aag	gct	gtc	ttc	cat	ctg	ccc	ggc	ata	1392	
Leu	Ile	Leu	Asp	Arg	Ile	Ala	Lys	Ala	Val	Phe	His	Leu	Pro	Gly	Ile		
				450			455				460						
ggg	ctg	gtg	cag	gcc	atg	acc	cg	ccg	cta	gga	acc	ccg	att	gac	cac	1440	
Gly	Leu	Val	Gln	Ala	Met	Thr	Arg	Pro	Leu	Gly	Thr	Pro	Ile	Asp	His		
465					470					475					480		
agc	tcg	ata	ccg	ttt	cag	atc	agc	atg	caa	agc	gtc	ggc	cag	att	cag	1488	
Ser	Ser	Ile	Pro	Phe	Gln	Ile	Ser	Met	Gln	Ser	Val	Gly	Gln	Ile	Gln		
				485				490						495			
aat	ctc	aag	tat	cag	agg	gac	cga	gca	gcc	gac	ttg	ctg	aag	cag	gcc	1536	
Asn	Leu	Lys	Tyr	Gln	Arg	Asp	Arg	Ala	Ala	Asp	Leu	Leu	Lys	Gln	Ala		
				500				505						510			
gaa	gag	ctg	ggg	aag	acg	atc	gaa	atc	ttg	cag	cg	caa	tat	gcc	cta	1584	
Glu	Glu	Leu	Gly	Lys	Thr	Ile	Glu	Ile	Leu	Gln	Arg	Gln	Tyr	Ala	Leu		
				515			520					525					
cag	cag	gaa	ctc	gcg	gcc	gct	act	cac	gag	caa	gcc	gaa	agc	ttt	cac	1632	
Gln	Gln	Glu	Leu	Ala	Ala	Thr	His	Glu	Gln	Ala	Glu	Glu	Ser	Phe	His		
				530			535				540						
caa	acg	atc	gcc	acg	gta	aag	gaa	ctg	cga	gat	agg	atc	gcc	aat	ttc	1680	
Gln	Thr	Ile	Ala	Thr	Val	Lys	Glu	Leu	Arg	Asp	Arg	Ile	Ala	Asn	Phe		
545					550					555					560		
gac	gat	ttc	ttc	agg	ccg	att	cgt	agt	tac	ttt	tac	tgg	gaa	aag	cac	1728	
Asp	Asp	Phe	Phe	Arg	Pro	Ile	Arg	Ser	Tyr	Phe	Tyr	Trp	Glu	Lys	His		
				565				570						575			
tgc	tac	gat	atc	ccg	agc	tgc	tgg	gcg	ctg							1758	
Cys	Tyr	Asp	Ile	Pro	Ser	Cys	Trp	Ala	Leu								
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<210> 8

<211> 586

<212> PRT

<213> Mycobacterium complex

<220>

<223> mmpL6 truncated protein

<400> 8

Met	Ser	Asn	His	His	Arg	Pro	Arg	Pro	Trp	Leu	Pro	His	Thr	Ile	Arg	1	5	10	15
Arg	Leu	Ser	Leu	Pro	Ile	Leu	Leu	Phe	Trp	Val	Gly	Val	Ala	Ala	Ile	20	25	30	
Thr	Asn	Ala	Ala	Val	Pro	Gln	Leu	Glu	Val	Val	Gly	Glu	Ala	His	Asn	35	40	45	
Val	Ala	Gln	Ser	Ser	Pro	Asp	Asp	Pro	Ser	Leu	Gln	Ala	Met	Lys	Arg	50	55	60	
Ile	Gly	Lys	Val	Phe	His	Glu	Phe	Asp	Ser	Asp	Ser	Ala	Ala	Met	Ile	65	70	75	80
Val	Leu	Glu	Gly	Asp	Lys	Pro	Leu	Gly	Asn	Asp	Ala	His	Arg	Phe	Tyr	85	90	95	
Asp	Thr	Leu	Leu	Arg	Asn	Leu	Ser	Asn	Asp	Thr	Lys	His	Val	Glu	His	100	105	110	
Val	Gln	Asp	Phe	Trp	Gly	Asp	Pro	Leu	Thr	Ala	Ala	Gly	Ser	Gln	Ser	115	120	125	
Thr	Asp	Gly	Lys	Ala	Ala	Tyr	Val	Gln	Val	Tyr	Leu	Ala	Gly	Asn	Gln	130	135	140	
Gly	Glu	Ala	Leu	Ser	Ile	Glu	Ser	Val	Asp	Ala	Val	Arg	Asp	Ile	Val	145	150	155	160
Ala	His	Thr	Pro	Pro	Pro	Ala	Gly	Val	Lys	Ala	Tyr	Val	Thr	Gly	Ala	165	170	175	
Ala	Pro	Leu	Met	Ala	Asp	Gln	Phe	Gln	Val	Gly	Ser	Lys	Gly	Thr	Ala	180	185	190	
Lys	Val	Thr	Gly	Ile	Thr	Leu	Val	Val	Ile	Ala	Val	Met	Leu	Leu	Phe	195	200	205	
Val	Tyr	Arg	Ser	Val	Val	Thr	Met	Val	Leu	Val	Leu	Ile	Thr	Val	Leu	210	215	220	
Ile	Glu	Leu	Ala	Ala	Ala	Arg	Gly	Ile	Val	Ala	Phe	Leu	Gly	Asn	Ala	225	230	235	240
Gly	Val	Ile	Gly	Leu	Ser	Thr	Tyr	Ser	Thr	Asn	Leu	Leu	Thr	Leu	Leu	245	250	255	
Val	Ile	Ala	Ala	Gly	Thr	Asp	Tyr	Ala	Ile	Phe	Val	Leu	Gly	Arg	Tyr	260	265	270	
His	Glu	Ala	Arg	Tyr	Ala	Ala	Gln	Asp	Arg	Glu	Thr	Ala	Phe	Tyr	Thr	275	280	285	
Met	Tyr	Arg	Gly	Thr	Ala	His	Val	Val	Leu	Gly	Ser	Gly	Leu	Thr	Val	290	295	300	

Ala Gly Ala Val Tyr Cys Leu Ser Phe Thr Arg Leu Pro Tyr Phe Gln
 305 310 315 320
 Ser Leu Gly Ile Pro Ala Ser Ile Gly Val Met Ile Ala Leu Ala Ala
 325 330 335
 Ala Leu Ser Leu Ala Pro Ser Val Leu Ile Leu Gly Ser Arg Phe Gly
 340 345 350
 Cys Phe Glu Pro Lys Arg Arg Met Arg Thr Arg Gly Trp Arg Arg Ile
 355 360 365
 Gly Thr Ala Ile Val Arg Trp Pro Gly Pro Ile Leu Ala Val Ala Cys
 370 375 380
 Ala Ile Ala Val Val Gly Leu Leu Ala Leu Pro Gly Tyr Lys Thr Ser
 385 390 395 400
 Tyr Asp Ala Arg Tyr Tyr Met Pro Ala Thr Ala Pro Ala Asn Ile Gly
 405 410 415
 Tyr Met Ala Ala Glu Arg His Phe Pro Gln Ala Arg Leu Asn Pro Glu
 420 425 430
 Leu Leu Met Ile Glu Thr Asp His Asp Met Arg Asn Pro Ala Asp Met
 435 440 445
 Leu Ile Leu Asp Arg Ile Ala Lys Ala Val Phe His Leu Pro Gly Ile
 450 455 460
 Gly Leu Val Gln Ala Met Thr Arg Pro Leu Gly Thr Pro Ile Asp His
 465 470 475 480
 Ser Ser Ile Pro Phe Gln Ile Ser Met Gln Ser Val Gly Gln Ile Gln
 485 490 495
 Asn Leu Lys Tyr Gln Arg Asp Arg Ala Ala Asp Leu Leu Lys Gln Ala
 500 505 510
 Glu Glu Leu Gly Lys Thr Ile Glu Ile Leu Gln Arg Gln Tyr Ala Leu
 515 520 525
 Gln Gln Glu Leu Ala Ala Ala Thr His Glu Gln Ala Glu Ser Phe His
 530 535 540
 Gln Thr Ile Ala Thr Val Lys Glu Leu Arg Asp Arg Ile Ala Asn Phe
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 Asp Asp Phe Phe Arg Pro Ile Arg Ser Tyr Phe Tyr Trp Glu Lys His
 565 570 575
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<210> 9

<211> 447

<212> DNA

<213> Mycobacterium complex

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<222> (1) .. (444)
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<223> mmpS6 coding sequence and protein

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Val	Gln	Gly	Ile	Ser	Val	Thr	Gly	Leu	Val	Lys	Arg	Gly	Trp	Met	Val	
1				5					10					15		

ctg gtt gcc gtg gcg gtg gtg gcg gtc gcg gga ttc agc gtc tat cgg 96
Leu Val Ala Val Ala Val Val Ala Val Ala Gly Phe Ser Val Tyr Arg
20 25 30

ttg	cac	ggc	atc	ttc	ggc	tcg	cac	gac	acc	acc	tcg	acc	gcc	ggt	ggt	144
Leu	His	Gly	Ile	Phe	Gly	Ser	His	Asp	Thr	Thr	Ser	Thr	Ala	Gly	Gly	
		35				40						45				

gtc gcg aac gac atc aag ccg ttc aac ccc aaa cag gta acc ctc gag 192
Val Ala Asn Asp Ile Lys Pro Phe Asn Pro Lys Gln Val Thr Leu Glu
50 55 60

gtc ttt ggc gct ccc gga acc gtg gca acg atc aat tat ctg gac gtg 240
Val Phe Gly Ala Pro Gly Thr Val Ala Thr Ile Asn Tyr Leu Asp Val
65 70 75 80

gat gcc aca cct cgg caa gtc ctg gac acg acc ctg cgg tgg tca tac 288
Asp Ala Thr Pro Arg Gln Val Leu Asp Thr Thr Leu Pro Trp Ser Tyr
85 90 95

acg atc acg acg acc ctg ccc gcg gtc ttc gcc aat gtt gtc gcg caa 336
Thr Ile Thr Thr Thr Leu Pro Ala Val Phe Ala Asn Val Val Ala Gln
100 105 110

ggc gac agc aat tcc atc ggc tgc cgc atc acc gtc aac ggt gta gtc 384
Gly Asp Ser Asn Ser Ile Gly Cys Arg Ile Thr Val Asn Gly Val Val
115 120 125

aag gac gaa agg atc gtc aac gaa gtg cgc gcc tat acc ttc tgc ctc 432
Lys Asp Glu Arg Ile Val Asn Glu Val Arg Ala Tyr Thr Phe Cys Leu
130 135 140

gac aag tcc tca tga . 447
Asp Lys Ser Ser
145

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<210> 10
<211> 148
<212> PRT
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<220>
<223> mmpS6 protein

<400> 10

Val Gln Gly Ile Ser Val Thr Gly Leu Val Lys Arg Gly Trp Met Val
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Leu Val Ala Val Ala Val Val Ala Val Ala Gly Phe Ser Val Tyr Arg
 20 25 30
 Leu His Gly Ile Phe Gly Ser His Asp Thr Thr Ser Thr Ala Gly Gly
 35 40 45
 Val Ala Asn Asp Ile Lys Pro Phe Asn Pro Lys Gln Val Thr Leu Glu
 50 55 60
 Val Phe Gly Ala Pro Gly Thr Val Ala Thr Ile Asn Tyr Leu Asp Val
 65 70 75 80
 Asp Ala Thr Pro Arg Gln Val Leu Asp Thr Thr Leu Pro Trp Ser Tyr
 85 90 95
 Thr Ile Thr Thr Thr Leu Pro Ala Val Phe Ala Asn Val Val Ala Gln
 100 105 110
 Gly Asp Ser Asn Ser Ile Gly Cys Arg Ile Thr Val Asn Gly Val Val
 115 120 125
 Lys Asp Glu Arg Ile Val Asn Glu Val Arg Ala Tyr Thr Phe Cys Leu
 130 135 140
 Asp Lys Ser Ser
 145

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<220>
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 <222> (1)..(399)

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 1 5 10 15
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 Leu His Gly Ile Phe Gly Ser His Asp Thr Thr Ser Thr Ala Gly Gly
 20 25 30
 gtc gcg aac gac atc aag ccg ttc aac ccc aaa cag gta acc ctc gag 144
 Val Ala Asn Asp Ile Lys Pro Phe Asn Pro Lys Gln Val Thr Leu Glu
 35 40 45
 gtc ttt ggc gct ccc gga acc gtg gca acg atc aat tat ctg gac gtg 192
 Val Phe Gly Ala Pro Gly Thr Val Ala Thr Ile Asn Tyr Leu Asp Val
 50 55 60
 gat gcc aca cct cgg caa gtc ctg gac acg acc ctg ccg tgg tca tac 240
 Asp Ala Thr Pro Arg Gln Val Leu Asp Thr Thr Leu Pro Trp Ser Tyr
 65 70 75 80

acg atc acg acg acc ctg ccc gcg gtc ttc gcc aat gtt gtc gcg caa 288
 Thr Ile Thr Thr Thr Leu Pro Ala Val Phe Ala Asn Val Val Ala Gln
 85 90 95

ggc gac agc aat tcc atc ggc tgc cgc atc acc gtc aac ggt gta gtc 336
 Gly Asp Ser Asn Ser Ile Gly Cys Arg Ile Thr Val Asn Gly Val Val
 100 105 110

aag gac gaa agg atc gtc aac gaa gtg cgc gcc tat acc ttc tgc ctc 384
 Lys Asp Glu Arg Ile Val Asn Glu Val Arg Ala Tyr Thr Phe Cys Leu
 115 120 125

gac aag tcc tca tga 399
 Asp Lys Ser Ser
 130

<210> 12

<211> 132

<212> PRT

<213> Mycobacterium complex

<220>

<223> mmpS6 truncated protein

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 1 5 10 15

Leu His Gly Ile Phe Gly Ser His Asp Thr Thr Ser Thr Ala Gly Gly
 20 25 30

Val Ala Asn Asp Ile Lys Pro Phe Asn Pro Lys Gln Val Thr Leu Glu
 35 40 45

Val Phe Gly Ala Pro Gly Thr Val Ala Thr Ile Asn Tyr Leu Asp Val
 50 55 60

Asp Ala Thr Pro Arg Gln Val Leu Asp Thr Thr Leu Pro Trp Ser Tyr
 65 70 75 80

Thr Ile Thr Thr Thr Leu Pro Ala Val Phe Ala Asn Val Val Ala Gln
 85 90 95

Gly Asp Ser Asn Ser Ile Gly Cys Arg Ile Thr Val Asn Gly Val Val
 100 105 110

Lys Asp Glu Arg Ile Val Asn Glu Val Arg Ala Tyr Thr Phe Cys Leu
 115 120 125

Asp Lys Ser Ser
 130

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<212> DNA

<213> Mycobacterium complex

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aatcgaactc gtggaacacc 20

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<400> 15
attcagcgtc tatcggttgc 20

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agcagctcgg gatatcgtag 20

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catagatccc ggacatggtg 20

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<222> (517)..(2307)

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caacacgaac	tgc ccaa acg	cttagaac tt	ggg ccgcagg	cgaaatcggt	ccagt cgccc	180
gagttcgccg	ctc gcttggc	tgccgctcaa	cacaggtagc	gcctaccagc	ctc gctgggt	240
tccatggcgt	gccccag tcc	gaagctgctg	ctgcttgact	ccgcgcgctg	ggccc gagcg	300
cgcgctgttg	tacggcccaa	acggcgtgtc	ggtgtacagt	cgcgcgctcg	cggttcagt	360
ccggcccccc	gactccggca	ggcccga cgg	cgcccagcgc	tagcccgaag	ttcccccttg	420
taggggcggg	ctg agtttcg	atctgtttcg	tgagcagg tg	tttctgtgtt	caacttcctt	480
caacatgtac	tcatgtatta	ttgagaatag	ctcggc	gtg Val 1	tca tcc tct Ser Ser Ser Asp Asp 5	534
gct att atc	gcg ctg acc	gcg tgt tat	aaa gta atc	atg tac att	acc	582
Ala Ile Ile	Ala Leu Thr	Ala Cys Tyr	Lys Val Ile	Met Tyr Ile	Thr	
	10		15		20	
cgg gta ccc	aac cgg gga	tcc ccg ccg	gcg gtg ctg	ttg cgg gaa	agc	630
Arg Val Pro	Asn Arg Gly	Ser Pro Pro	Ala Val Leu	Leu Arg Glu	Ser	
	25		30		35	
ttc cgc gaa	aac gcc aag	gtc aag acg	cgt acc ctg	gcc aac ctc	tca	678
Phe Arg Glu	Asn Gly Lys	Val Lys Thr	Arg Thr Leu	Ala Asn Leu	Ser	
	40		45		50	
cgc tgg ccc	gag cac aag	ctg gac aga	ctg gac cgg	gcg ctt aag	ggc	726
Arg Trp Pro	Glu His Lys	Leu Asp Arg	Leu Asp Arg	Ala Leu Lys	Gly	
	55		60		65	70
ttg ccg ccc	gcg gac tgg	gat cta gcc	gag gcc ttc	gat atc acc	cg	774
Leu Pro Pro	Ala Asp Trp	Asp Leu Ala	Glu Ala Phe	Asp Ile Thr	Arg	
		75		80	85	
agc ctg ccg	cac ggg cat	gtg gcc gcg	gtg gcc ggc	acc gcc gag	aag	822
Ser Leu Pro	His Gly His	Val Ala Ala	Val Ala Gly	Thr Ala Glu	Lys	
	90		95		100	
ctg ggc ata	ccc gag ctg	atc gac ccc	acc ccg tcg	cg	cg	870
Leu Gly Ile	Pro Glu Leu	Ile Asp Pro	Thr Pro Ser	Arg Arg Arg	Asn	
	105		110		115	
ctg gtg ctg	gcc atg ctg	atc ggg cag	atc atc gag	ccc gga tcg	aaa	918
Leu Val Leu	Ala Met Leu	Ile Gly Gln	Ile Ile Glu	Pro Gly Ser	Lys	
	120		125		130	
ctg gcg atc	gcg cgc ggg	ctg cgc gcc	cag acc gcc	acc agc acg	ctg	966
Leu Ala Ile	Ala Arg Gly	Leu Arg Ala	Gln Thr Ala	Thr Ser Thr	Leu	
	135		140		145	150
ggt gcg gtg	ctg ggt gtc	tcg ggc gcc	gat gag gac	gac ctg tat	gac	1014
Gly Ala Val	Leu Gly Val	Ser Gly Ala	Asp Glu Asp	Asp Leu Tyr	Asp	
	155		160		165	
gcg atg gac	tgg gcg ctg	gag gcg aaa	gac ggc atc	gaa aac gcc	ttg	1062
Ala Met Asp	Trp Ala Leu	Glu Arg Lys	Asp Gly Ile	Glu Asn Ala	Leu	
	170		175		180	

gcc gca cgg cat ctg acc aac ggc acc ctg gtg ctc tat gac gta tcc	1110
Ala Ala Arg His Leu Thr Asn Gly Thr Leu Val Leu Tyr Asp Val Ser	
185 190 195	
tcg gcg gcg ttc gag ggc cac acc tgc ccg ctg gga gcg atc ggg cac	1158
Ser Ala Ala Phe Glu Gly His Thr Cys Pro Leu Gly Ala Ile Gly His	
200 205 210	
gcc cgc gac ggg gtc aaa ggc cgg ctg cag atc gtc tac ggg ctg ctg	1206
Ala Arg Asp Gly Val Lys Gly Arg Leu Gln Ile Val Tyr Gly Leu Leu	
215 220 225 230	
tgc tca ccc aag gga gcg ccg gtg gcc atc gag gtg ttc aag ggc aac	1254
Cys Ser Pro Lys Gly Ala Pro Val Ala Ile Glu Val Phe Lys Gly Asn	
235 240 245	
acc gcc gac ccg aaa act ctg aaa gct caa atc gac aag ctc aaa acc	1302
Thr Ala Asp Pro Lys Thr Leu Lys Ala Gln Ile Asp Lys Leu Lys Thr	
250 255 260	
cgg ttc ggg ttg acc cgc atc gcc ctg gtg ggc gat cgg ggc atg ctc	1350
Arg Phe Gly Leu Thr Arg Ile Ala Leu Val Gly Asp Arg Gly Met Leu	
265 270 275	
act tcc gcg cgc atc cgt gac gag ctg cgt ccg gcg cac ctg gat tgg	1398
Thr Ser Ala Arg Ile Arg Asp Glu Leu Arg Pro Ala His Leu Asp Trp	
280 285 290	
atc agc gcg ctg cgc gcc ccg cag atc aag atc ctg ctc gag gac ggg	1446
Ile Ser Ala Leu Arg Ala Pro Gln Ile Lys Ile Leu Leu Glu Asp Gly	
295 300 305 310	
gcg ctg cag ctg tcg ctg ttc gat gag cag aac ctg ttc gag atc act	1494
Ala Leu Gln Leu Ser Leu Phe Asp Glu Gln Asn Leu Phe Glu Ile Thr	
315 320 325	
cac ccc gac tat ccc ggt gag cgg ctg gtg tgc tgc cac aac ccc gcc	1542
His Pro Asp Tyr Pro Gly Glu Arg Leu Val Cys Cys His Asn Pro Ala	
330 335 340	
ctg gcc gac gag cgc gcc cgc aaa cgc gcc gag ctg ctg gcg gcc acc	1590
Leu Ala Asp Glu Arg Ala Arg Lys Arg Ala Glu Leu Leu Ala Ala Thr	
345 350 355	
gaa aag gag ctg cag gcc atc gcc gaa gcc acc cgc cgc caa cgc cgg	1638
Glu Lys Glu Leu Gln Ala Ile Ala Glu Ala Thr Arg Arg Gln Arg Arg	
360 365 370	
ccg tta cgc ggt aca gac aag atc ggc ctg cgg gtg ggc aag gtg cgc	1686
Pro Leu Arg Gly Thr Asp Lys Ile Gly Leu Arg Val Gly Lys Val Arg	
375 380 385 390	
aac aag ttc aag atg gcc aag cac ttt gac ctg cac atc acc gat gag	1734
Asn Lys Phe Lys Met Ala Lys His Phe Asp Leu His Ile Thr Asp Glu	
395 400 405	
gcc ttc agc ttc acc cgc aac cag aac agt atc gcc gcc gag gcc gcc	1782
Ala Phe Ser Phe Thr Arg Asn Gln Asn Ser Ile Ala Ala Glu Ala Ala	
410 415 420	

ctc gac ggc atc tac gtg cta cgc acc agc ctg ccc gac aac gcc ctg 1830
 Leu Asp Gly Ile Tyr Val Leu Arg Thr Ser Leu Pro Asp Asn Ala Leu
 425 430 435
 ggc cgc gac gac gtg gtg ggc cgc tac aaa gac ctc gcc gac gtc gaa 1878
 Gly Arg Asp Asp Val Val Gly Arg Tyr Lys Asp Leu Ala Asp Val Glu
 440 445 450
 cgc ttc ttc cgc acc ctc aac agc gaa ctg gac gta cgc ccc atc cgg 1926
 Arg Phe Phe Arg Thr Leu Asn Ser Glu Leu Asp Val Arg Pro Ile Arg
 455 460 465 470
 cat cgg ctg gcc gac cgg gtc cgc gcc cac atg ttc ttg cac atg ctc 1974
 His Arg Leu Ala Asp Arg Val Arg Ala His Met Phe Leu His Met Leu
 475 480 485
 tcc tac tac atc agc tgg cac atg aaa caa gcc ctg gcc cca atc ctg 2022
 Ser Tyr Tyr Ile Ser Trp His Met Lys Gln Ala Leu Ala Pro Ile Leu
 490 495 500
 ttc acc gac aac gac aaa ccc gcc gcc gcc gcc aaa cgc gcc gac ccc 2070
 Phe Thr Asp Asn Asp Lys Pro Ala Ala Ala Lys Arg Ala Asp Pro
 505 510 515
 gtc gcg cca gcc caa cgc tcc gac gaa gcg ctg aac aag gca gca cgc 2118
 Val Ala Pro Ala Gln Arg Ser Asp Glu Ala Leu Asn Lys Ala Ala Arg
 520 525 530
 aaa cgc acc gaa gac aac caa ccg gtg cac agc ttc acc agc ctg ctc 2166
 Lys Arg Thr Glu Asp Asn Gln Pro Val His Ser Phe Thr Ser Leu Leu
 535 540 545 550
 acc gac ctg gcc acc atc tgc gcc aac tac atc caa ccc aca gac gac 2214
 Thr Asp Leu Ala Thr Ile Cys Ala Asn Tyr Ile Gln Pro Thr Asp Asp
 555 560 565
 ctg cca gca ttc acc aaa acc acc acc ccc acc ccc aca caa cgg cgc 2262
 Leu Pro Ala Phe Thr Lys Thr Thr Thr Pro Thr Pro Thr Gln Arg Arg
 570 575 580
 gcc ttc gac cta ctg gcc gtt tcc cac cgc cac ggc ctg gcg tag 2307
 Ala Phe Asp Leu Leu Ala Val Ser His Arg His Gly Leu Ala
 585 590 595
 tcagtaccga accacaaatg cccaggtcaa cgacacaaac cgcgccggat cagggggaac 2367
 ttcgggctag cccggcgcgc cgg 2390

<210> 20

<211> 596

<212> PRT

<213> *Mycobacterium canettii*

<400> 20

Val Ser Ser Ser Asp Asp Ala Ile Ile Ala Leu Thr Ala Cys Tyr Lys
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Val Ile Met Tyr Ile Thr Arg Val Pro Asn Arg Gly Ser Pro Pro Ala
 20 25 30

Val Leu Leu Arg Glu Ser Phe Arg Glu Asn Gly Lys Val Lys Thr Arg
 35 40 45
 Thr Leu Ala Asn Leu Ser Arg Trp Pro Glu His Lys Leu Asp Arg Leu
 50 55 60
 Asp Arg Ala Leu Lys Gly Leu Pro Pro Ala Asp Trp Asp Leu Ala Glu
 65 70 75 80
 Ala Phe Asp Ile Thr Arg Ser Leu Pro His Gly His Val Ala Ala Val
 85 90 95
 Ala Gly Thr Ala Glu Lys Leu Gly Ile Pro Glu Leu Ile Asp Pro Thr
 100 105 110
 Pro Ser Arg Arg Arg Asn Leu Val Leu Ala Met Leu Ile Gly Gln Ile
 115 120 125
 Ile Glu Pro Gly Ser Lys Leu Ala Ile Ala Arg Gly Leu Arg Ala Gln
 130 135 140
 Thr Ala Thr Ser Thr Leu Gly Ala Val Leu Gly Val Ser Gly Ala Asp
 145 150 155 160
 Glu Asp Asp Leu Tyr Asp Ala Met Asp Trp Ala Leu Glu Arg Lys Asp
 165 170 175
 Gly Ile Glu Asn Ala Leu Ala Ala Arg His Leu Thr Asn Gly Thr Leu
 180 185 190
 Val Leu Tyr Asp Val Ser Ser Ala Ala Phe Glu Gly His Thr Cys Pro
 195 200 205
 Leu Gly Ala Ile Gly His Ala Arg Asp Gly Val Lys Gly Arg Leu Gln
 210 215 220
 Ile Val Tyr Gly Leu Leu Cys Ser Pro Lys Gly Ala Pro Val Ala Ile
 225 230 235 240
 Glu Val Phe Lys Gly Asn Thr Ala Asp Pro Lys Thr Leu Lys Ala Gln
 245 250 255
 Ile Asp Lys Leu Lys Thr Arg Phe Gly Leu Thr Arg Ile Ala Leu Val
 260 265 270
 Gly Asp Arg Gly Met Leu Thr Ser Ala Arg Ile Arg Asp Glu Leu Arg
 275 280 285
 Pro Ala His Leu Asp Trp Ile Ser Ala Leu Arg Ala Pro Gln Ile Lys
 290 295 300
 Ile Leu Leu Glu Asp Gly Ala Leu Gln Leu Ser Leu Phe Asp Glu Gln
 305 310 315 320
 Asn Leu Phe Glu Ile Thr His Pro Asp Tyr Pro Gly Glu Arg Leu Val
 325 330 335
 Cys Cys His Asn Pro Ala Leu Ala Asp Glu Arg Ala Arg Lys Arg Ala
 340 345 350
 Glu Leu Leu Ala Ala Thr Glu Lys Glu Leu Gln Ala Ile Ala Glu Ala

355					360					365					
Thr	Arg	Arg	Gln	Arg	Arg	Pro	Leu	Arg	Gly	Thr	Asp	Lys	Ile	Gly	Leu
370						375					380				
Arg	Val	Gly	Lys	Val	Arg	Asn	Lys	Phe	Lys	Met	Ala	Lys	His	Phe	Asp
385					390					395					400
Leu	His	Ile	Thr	Asp	Glu	Ala	Phe	Ser	Phe	Thr	Arg	Asn	Gln	Asn	Ser
				405					410					415	
Ile	Ala	Ala	Glu	Ala	Ala	Leu	Asp	Gly	Ile	Tyr	Val	Leu	Arg	Thr	Ser
			420					425					430		
Leu	Pro	Asp	Asn	Ala	Leu	Gly	Arg	Asp	Asp	Val	Val	Gly	Arg	Tyr	Lys
		435					440					445			
Asp	Leu	Ala	Asp	Val	Glu	Arg	Phe	Phe	Arg	Thr	Leu	Asn	Ser	Glu	Leu
	450					455					460				
Asp	Val	Arg	Pro	Ile	Arg	His	Arg	Leu	Ala	Asp	Arg	Val	Arg	Ala	His
465					470					475					480
Met	Phe	Leu	His	Met	Leu	Ser	Tyr	Tyr	Ile	Ser	Trp	His	Met	Lys	Gln
				485					490					495	
Ala	Leu	Ala	Pro	Ile	Leu	Phe	Thr	Asp	Asn	Asp	Lys	Pro	Ala	Ala	Ala
			500					505					510		
Ala	Lys	Arg	Ala	Asp	Pro	Val	Ala	Pro	Ala	Gln	Arg	Ser	Asp	Glu	Ala
			515				520					525			
Leu	Asn	Lys	Ala	Ala	Arg	Lys	Arg	Thr	Glu	Asp	Asn	Gln	Pro	Val	His
	530					535					540				
Ser	Phe	Thr	Ser	Leu	Leu	Thr	Asp	Leu	Ala	Thr	Ile	Cys	Ala	Asn	Tyr
545					550					555					560
Ile	Gln	Pro	Thr	Asp	Asp	Leu	Pro	Ala	Phe	Thr	Lys	Thr	Thr	Thr	Pro
				565				570						575	
Thr	Pro	Thr	Gln	Arg	Arg	Ala	Phe	Asp	Leu	Leu	Ala	Val	Ser	His	Arg
			580					585					590		
His	Gly	Leu	Ala												
		595													

<210> 21
 <211> 1191
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <221> CDS
 <222> (1)..(1191)
 <223> Fusion gene between mmpS6 and mmpL6 genes

<220>
 <221> misc_feature
 <222> (1) (1191)

<223> CDS corresponds to fusion protein of rearranged forms
of mmpS6 and mmpL6

<400> 1

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Val Gln Gly Ile Ser Val Thr Gly Leu Val Lys Arg Gly Trp Met Val	
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aga tcc gtc ttt gac acg atc gac ggt atc gac caa ctc ggc gag cag	96
Arg Ser Val Phe Asp Thr Ile Asp Gly Ile Asp Gln Leu Gly Glu Gln	
20 25 30	
ctg gcc agc gtg acc gta acc ttg gac aag ttg gct gcg atc cag cct	144
Leu Ala Ser Val Thr Val Thr Leu Asp Lys Leu Ala Ala Ile Gln Pro	
35 40 45	
caa ttg gtg gcg ctg cta cca gac gag atc gcc agc cag cag atc aat	192
Gln Leu Val Ala Leu Leu Pro Asp Glu Ile Ala Ser Gln Gln Ile Asn	
50 55 60	
cgg gaa ctg gcg ctg gct aac tac gcc acc atg tcc ggg atc tat gcc	240
Arg Glu Leu Ala Leu Ala Asn Tyr Ala Thr Met Ser Gly Ile Tyr Ala	
65 70 75 80	
cag acg gcg gcc ttg atc gaa aac gct gcc gcc atg gga caa gcc ttt	288
Gln Thr Ala Ala Leu Ile Glu Asn Ala Ala Ala Met Gly Gln Ala Phe	
85 90 95	
gac gcc gcc aag aac gac gac tcc ttc tat ctg ccg ccg gag gct ttt	336
Asp Ala Ala Lys Asn Asp Asp Ser Phe Tyr Leu Pro Pro Glu Ala Phe	
100 105 110	
gac aac cca gat ttc cag cgc ggc ctg aaa ttg ttc ctg tcg gca gac	384
Asp Asn Pro Asp Phe Gln Arg Gly Leu Lys Leu Phe Leu Ser Ala Asp	
115 120 125	
ggt aag gcg gct cgg atg atc atc tcc cat gaa ggc gat ccc gcc acc	432
Gly Lys Ala Ala Arg Met Ile Ile Ser His Glu Gly Asp Pro Ala Thr	
130 135 140	
ccc gaa ggc att tcg cat atc gac gcg atc aag cag gcg gcc cac gag	480
Pro Glu Gly Ile Ser His Ile Asp Ala Ile Lys Gln Ala Ala His Glu	
145 150 155 160	
gcc gtg aag ggc act ccc atg gcg ggt gct ggg atc tat ctg gcc ggc	528
Ala Val Lys Gly Thr Pro Met Ala Gly Ala Gly Ile Tyr Leu Ala Gly	
165 170 175	
acg gcc gcc acc ttc aag gac att caa gac ggc gcc acc tac gac ctc	576
Thr Ala Ala Thr Phe Lys Asp Ile Gln Asp Gly Ala Thr Tyr Asp Leu	
180 185 190	
ctg atc gcc gga ata gcc gcg ctg agc ttg att ttg ctc atc atg atg	624
Leu Ile Ala Gly Ile Ala Ala Leu Ser Leu Ile Leu Leu Ile Met Met	
195 200 205	
atc att acc cga agc ctg gtt gcg gcg ctg gtg atc gtg ggc acg gtg	672
Ile Ile Thr Arg Ser Leu Val Ala Ala Leu Val Ile Val Gly Thr Val	
210 215 220	

gcg ctg tcg ttg ggc gct tct ttt ggc ctg tcc gtg ctg gtg tgg cag	720
Ala Leu Ser Leu Gly Ala Ser Phe Gly Leu Ser Val Leu Val Trp Gln	
225 230 235 240	
cat ctt ctc ggt atc cag ttg tac tgg atc gtg ctc gcg ctg gcc gtc	768
His Leu Leu Gly Ile Gln Leu Tyr Trp Ile Val Leu Ala Leu Ala Val	
245 250 255	
atc ctg ctc ctg gcc gtg gga tgc gac tat aac ttg ctg ctg att tcc	816
Ile Leu Leu Leu Ala Val Gly Ser Asp Tyr Asn Leu Leu Leu Ile Ser	
260 265 270	
cga ttc aag gag gag atc ggt gca ggt ttg aac acc gcc atc atc cgt	864
Arg Phe Lys Glu Glu Ile Gly Ala Gly Leu Asn Thr Gly Ile Ile Arg	
275 280 285	
gcg atg gcc ggc acc ggc ggg gtg gtg acc gct gcc ggc ctg gtg ttc	912
Ala Met Ala Gly Thr Gly Gly Val Val Thr Ala Ala Gly Leu Val Phe	
290 295 300	
gcc gcc act atg tct tgc ttc gtg ttc agt gat ttg cgg gtc ctc ggt	960
Ala Ala Thr Met Ser Ser Phe Val Phe Ser Asp Leu Arg Val Leu Gly	
305 310 315 320	
cag atc ggg acc acc att ggt ctt ggg ctg ctg ttc gac acg ctg gtg	1008
Gln Ile Gly Thr Thr Ile Gly Leu Gly Leu Leu Phe Asp Thr Leu Val	
325 330 335	
gtg cgc gcg ttc atg acc ccg tcc atc gcg gtg ctg ctc ggg cgc tgg	1056
Val Arg Ala Phe Met Thr Pro Ser Ile Ala Val Leu Leu Gly Arg Trp	
340 345 350	
ttc tgg tgg ccg caa cga gtg cgc ccg cgc cct gcc agc agg atg ctt	1104
Phe Trp Trp Pro Gln Arg Val Arg Pro Arg Pro Ala Ser Arg Met Leu	
355 360 365	
cgg ccg tac ggc ccg cgg ccc gtg gtt cgt gaa ttg ctg ctg cgc gag	1152
Arg Pro Tyr Gly Pro Arg Pro Val Val Arg Glu Leu Leu Leu Arg Glu	
370 375 380	
ggc aac gat gac ccg aga act cag gtg gct acc cac cgt	1191
Gly Asn Asp Asp Pro Arg Thr Gln Val Ala Thr His Arg	
385 390 395	

<210> 22

<211> 397

<212> PRT

<213> Mycobacterium tuberculosis

<220>

<223> Fusion protein of rearranged forms of mmpS6 and mmpL6

<400> 2

Val	Gln	Gly	Ile	Ser	Val	Thr	Gly	Leu	Val	Lys	Arg	Gly	Trp	Met	Val
1				5				10						15	

Arg	Ser	Val	Phe	Asp	Thr	Ile	Asp	Gly	Ile	Asp	Gln	Leu	Gly	Glu	Gln
			20					25					30		

Leu Ala Ser Val Thr Val Thr Leu Asp Lys Leu Ala Ala Ile Gln Pro
 35 40 45
 Gln Leu Val Ala Leu Leu Pro Asp Glu Ile Ala Ser Gln Gln Ile Asn
 50 55 60
 Arg Glu Leu Ala Leu Ala Asn Tyr Ala Thr Met Ser Gly Ile Tyr Ala
 65 70 75 80
 Gln Thr Ala Ala Leu Ile Glu Asn Ala Ala Ala Met Gly Gln Ala Phe
 85 90 95
 Asp Ala Ala Lys Asn Asp Asp Ser Phe Tyr Leu Pro Pro Glu Ala Phe
 100 105 110
 Asp Asn Pro Asp Phe Gln Arg Gly Leu Lys Leu Phe Leu Ser Ala Asp
 115 120 125
 Gly Lys Ala Ala Arg Met Ile Ile Ser His Glu Gly Asp Pro Ala Thr
 130 135 140
 Pro Glu Gly Ile Ser His Ile Asp Ala Ile Lys Gln Ala Ala His Glu
 145 150 155 160
 Ala Val Lys Gly Thr Pro Met Ala Gly Ala Gly Ile Tyr Leu Ala Gly
 165 170 175
 Thr Ala Ala Thr Phe Lys Asp Ile Gln Asp Gly Ala Thr Tyr Asp Leu
 180 185 190
 Leu Ile Ala Gly Ile Ala Ala Leu Ser Leu Ile Leu Leu Ile Met Met
 195 200 205
 Ile Ile Thr Arg Ser Leu Val Ala Ala Leu Val Ile Val Gly Thr Val
 210 215 220
 Ala Leu Ser Leu Gly Ala Ser Phe Gly Leu Ser Val Leu Val Trp Gln
 225 230 235 240
 His Leu Leu Gly Ile Gln Leu Tyr Trp Ile Val Leu Ala Leu Ala Val
 245 250 255
 Ile Leu Leu Leu Ala Val Gly Ser Asp Tyr Asn Leu Leu Leu Ile Ser
 260 265 270
 Arg Phe Lys Glu Glu Ile Gly Ala Gly Leu Asn Thr Gly Ile Ile Arg
 275 280 285
 Ala Met Ala Gly Thr Gly Gly Val Val Thr Ala Ala Gly Leu Val Phe
 290 295 300
 Ala Ala Thr Met Ser Ser Phe Val Phe Ser Asp Leu Arg Val Leu Gly
 305 310 315 320
 Gln Ile Gly Thr Thr Ile Gly Leu Gly Leu Leu Phe Asp Thr Leu Val
 325 330 335
 Val Arg Ala Phe Met Thr Pro Ser Ile Ala Val Leu Leu Gly Arg Trp
 340 345 350

Phe Trp Trp Pro Gln Arg Val Arg Pro Arg Pro Ala Ser Arg Met Leu
355 360 365

Arg Pro Tyr Gly Pro Arg Pro Val Val Arg Glu Leu Leu Leu Arg Glu
370 375 380

Gly Asn Asp Asp Pro Arg Thr Gln Val Ala Thr His Arg
385 390 395